deleted from formula (I), wherein a helical turn consists of 3 to 4 consecutive residues selected from residues X_1 to X_{23} of formula (I):

$$Z_1\text{-}X_1\text{-}X_2\text{-}X_3\text{-}X_4\text{-}X_5\text{-}X_6\text{-}X_7\text{-}X_8\text{-}X_9\text{-}X_{10}\text{-}X_{11}\text{-}X_{12}\text{-}X_{13}\text{-}X_{14}\text{-}X_{15}\text{-}X_{16}\text{-}X_{17}\text{-}X_{18}\text{-}X_{19}\text{-}X_{20}\text{-}X_{21}\text{-}X_{22}\text{-}X_{23}\text{-}Z_2$$

or a pharmaceutically acceptable salt thereof, wherein:

X_1 is Pro (P), Ala (A), Gly (G), Gln (Q), Asn (N), Asp (D) or D-Pro (p);

X_2 is an aliphatic residue;

X_3 is a Leu (L) or Phe (F);

X_4 is Glu (E);

X_5 is an aliphatic residue;

X_6 is Leu (L) or Phe (F);

X_7 is Glu (E) or Leu (L);

X_8 is Asn (N) or Gln (Q);

X_9 is Leu (L);

X_{10} is Leu (L), Trp (W) or Gly (G);

X_{11} is an acidic residue;

X_{12} is Arg (R);

D1 cont'd

X_{13} is Leu (L) or Gly (G);

X_{14} is Leu (L), Phe (F) or Gly (G);

X_{15} is Asp (D);

X_{16} is Ala (A);

X_{17} is Leu (L);

X_{18} is Asn (N) or Gln (Q);

X_{19} is a basic residue;

X_{20} is a basic residue;

X_{21} is Leu (L);

X_{22} is a basic residue;

X_{23} is absent or a basic residue;

Z_1 is H_2N- ;

Z_2 is -C (O) NRR or -C (O) OR;

each R is independently -H, (C_1-C_6) alkyl, (C_1-C_6) alkenyl, (C_1-C_6) alkynyl, (C_5-C_{20}) aryl, (C_6-C_{26}) alkaryl, 5-20 membered heteroaryl or 6-26 membered alkheteroaryl or a 1 to 7-residue peptide or peptide analogue in which one more bonds between residues 1-7 are independently a substituted amide, an isostere of an amide or an amide mimetic; and

each "-" between residues X_1 to X_{23} and between residues of the peptide to Z_2 independently designates an amide linkage, a substituted amide linkage, an isostere of an amide or an amide mimetic; or

an N- terminally blocked form, a C-terminally blocked form, or an N- and C-terminally blocked form of formula (I).

D1 cont

56. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1, in which one helical turn is deleted.

57. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1, in which three, four, six, seven or eight residues X_1 , X_2 , X_3 , X_4 , X_5 , X_6 , X_7 , X_8 , X_9 , X_{10} , X_{11} , X_{12} , X_{13} , X_{14} , X_{15} , X_{16} , X_{17} , X_{18} , X_{19} , X_{20} , X_{21} and X_{22} are deleted.

D2

58. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 57, in which 3 consecutive residues are deleted.

59. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 57, in which 4 consecutive residues are deleted.

60. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 57, in which two non-contiguous sets of 3 consecutive residues are deleted.

61. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 57, in which two non-contiguous sets of 4 consecutive residues are deleted.

62. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 57, in which one set of 3 consecutive residues and one set of 4 consecutive residues are deleted.

D2 cont

63. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 57, in which 6, 7 or 8 consecutive residues are deleted.

67. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1 in which:
the "-" between residues designates -C (O) NH- ;
Z_1 is H_2N- ; and
Z_2 is -C (O) OH or a salt thereof.

68. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1, in which the mean hydrophobic moment, $<\mu_H>$, is 0.45 to 0.65.

69. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 68, in which the mean hydrophobic moment, $<\mu_H>$, is 0.50 to 0.60.

D3

70. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1, in which the mean hydrophobicity, $<H_o>$, is -0.050 to -0.070.

71. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1, in which the mean hydrophobicity, $<H_o>$, is -0.030 to -0.055.

72. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1, in which the mean hydrophobicity of the hydrophobic face, $<H_o^{pho}>$, is 0.90 to 1.20.

73. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 72, in which the mean hydrophobicity of the hydrophobic face, $<H_o^{pho}>$, is 0.94 to 1.10.

74. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 1, in which the pho angle is 160° to 220°.

75. (Amended) The 15 to 26-residue peptide or peptide analogue of Claim 74, in which the pho angle is 180° to 200°.

79. (Amended) A pharmaceutical composition comprising an ApoA-I agonist compound and a pharmaceutically acceptable carrier, excipient or diluent, wherein the ApoA-I agonist compound is a 15 to 26- residue peptide or peptide analogue according to Claim 1 or 57.

D4

82. (Amended) The pharmaceutical composition of Claim 79 which is a lyophilized powder.

D5

83. (Amended) The pharmaceutical composition of Claim 79 which is a solution.

Please add new Claims 84-88:

84. (New) The N-terminally blocked form of the 15 to 26-residue peptide or peptide analogue of Claim 1.

85. (New) The 15 to 26-residue peptide or peptide analogue of Claim 84 in which the N-terminally blocking group is selected from the group consisting of acetyl, formyl and dansyl.

D6

86. (New) The C-terminally blocked form of the 15 to 26-residue peptide or peptide analogue of Claim 1.

87. (New) The 15 to 26-residue peptide or peptide analogue of Claim 86 in which the C-terminally blocking group is methyl.

88. (New) The N-terminally and C-terminally blocked form of the 15 to 26-residue peptide or peptide analogue of Claim 1.